

FIG.1

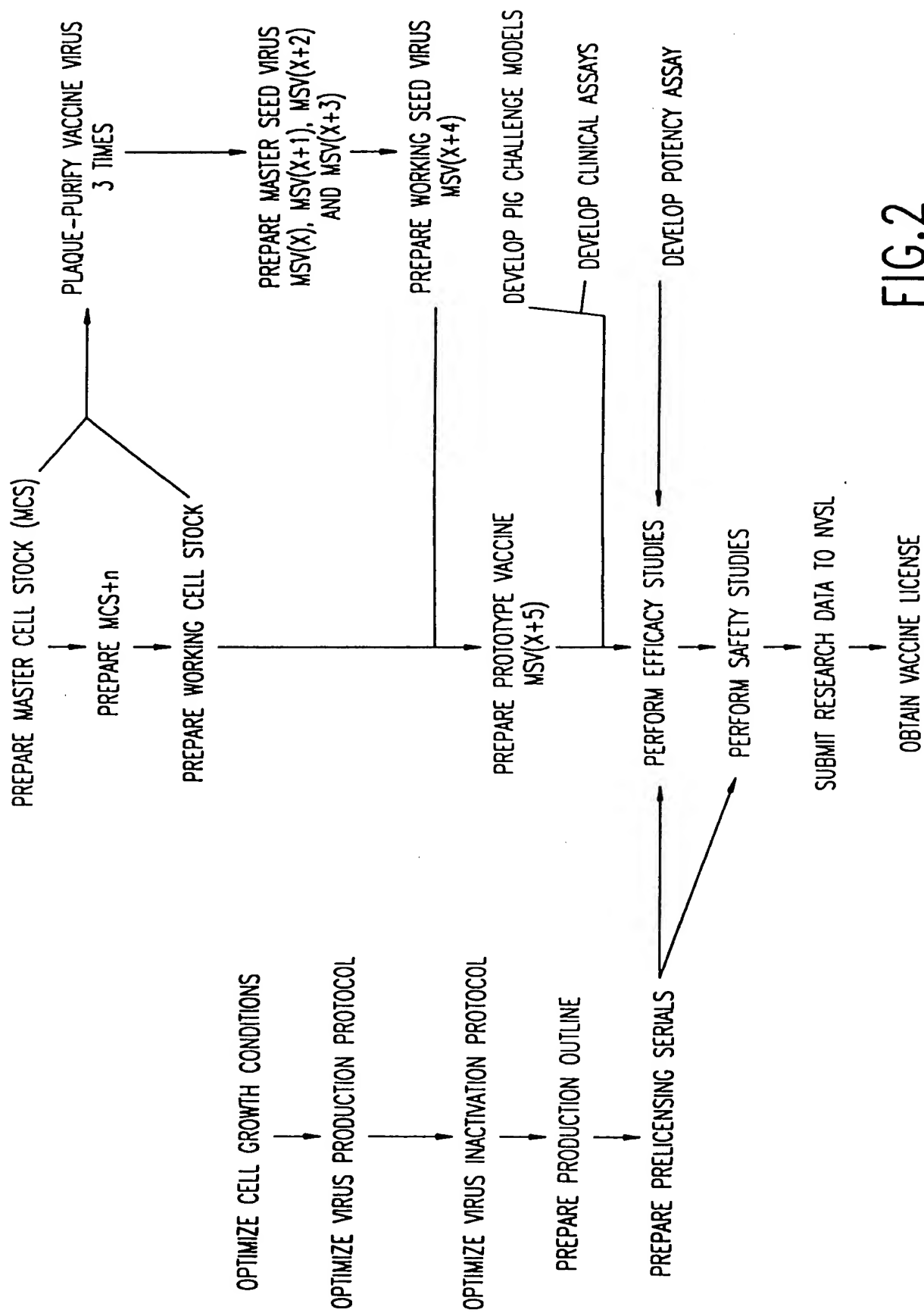
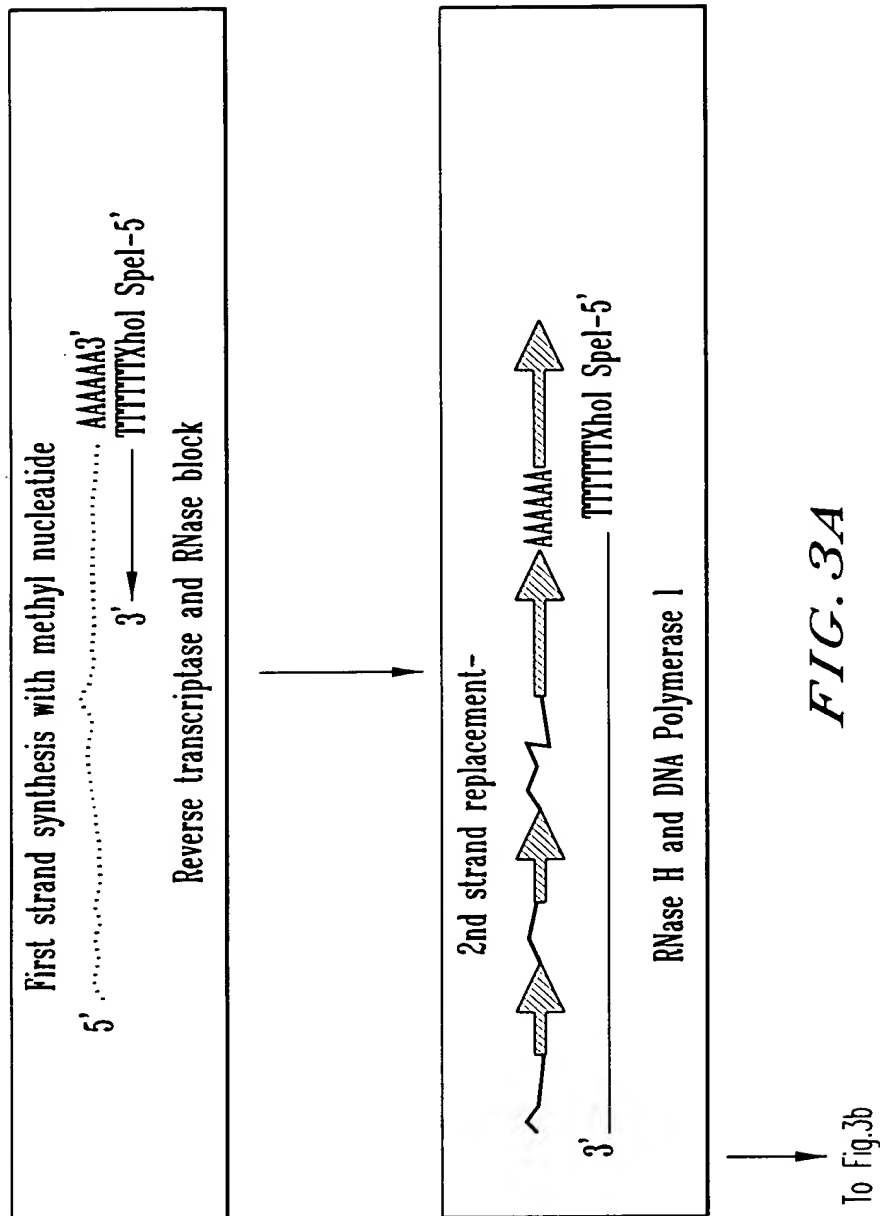


FIG. 2



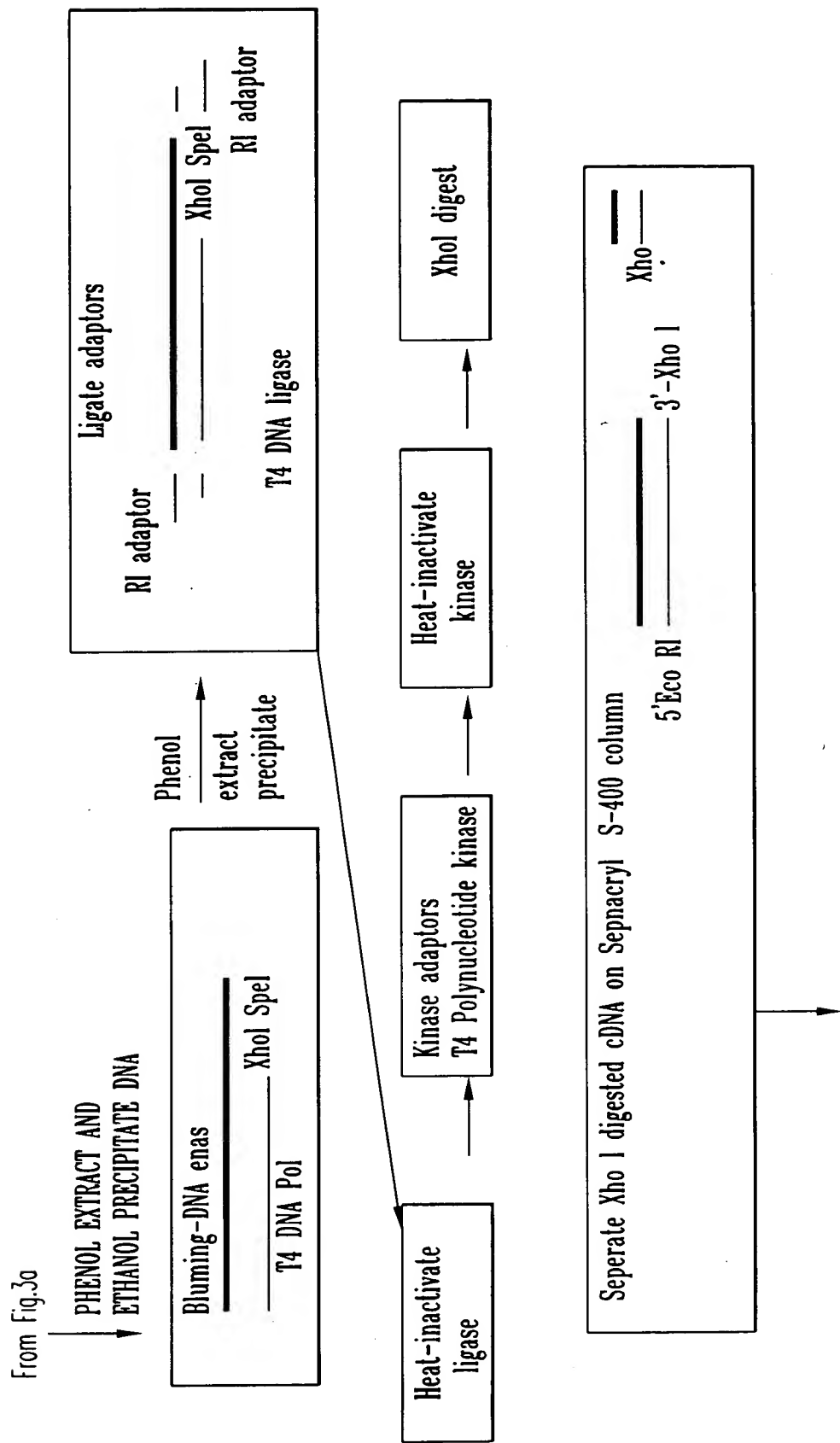


FIG. 3B

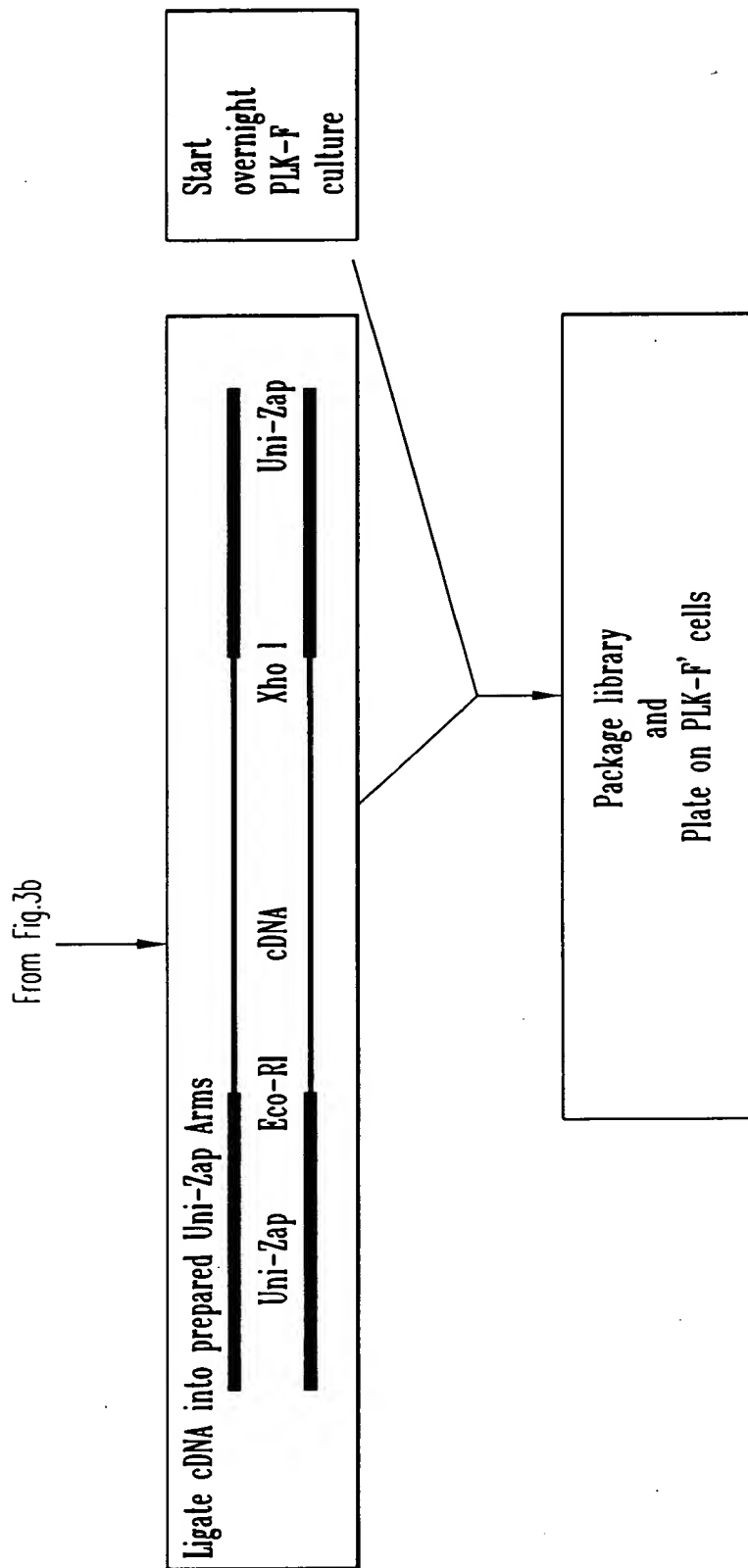


FIG. 3c

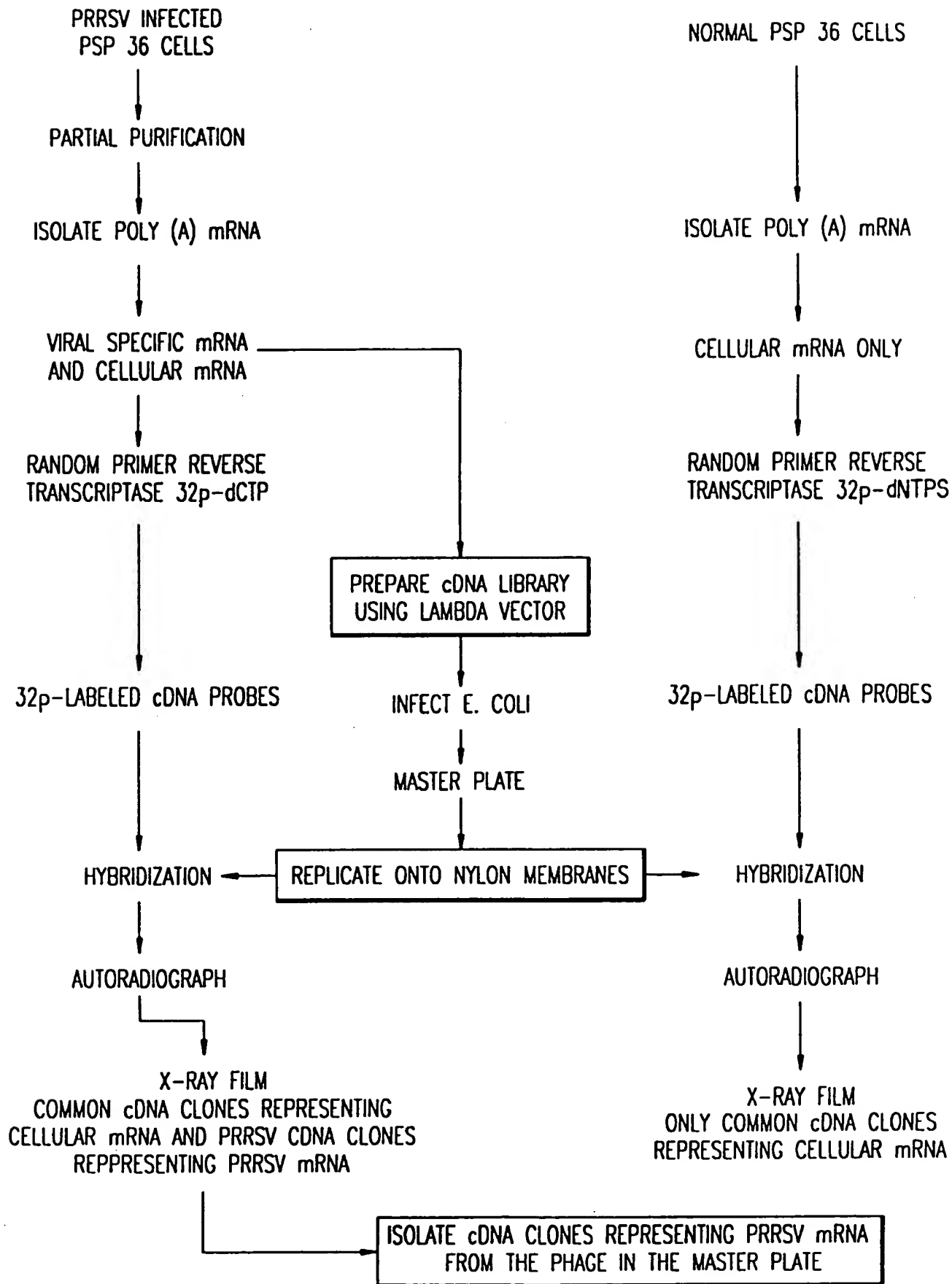


FIG.4

FOOTED TOSOTBOD

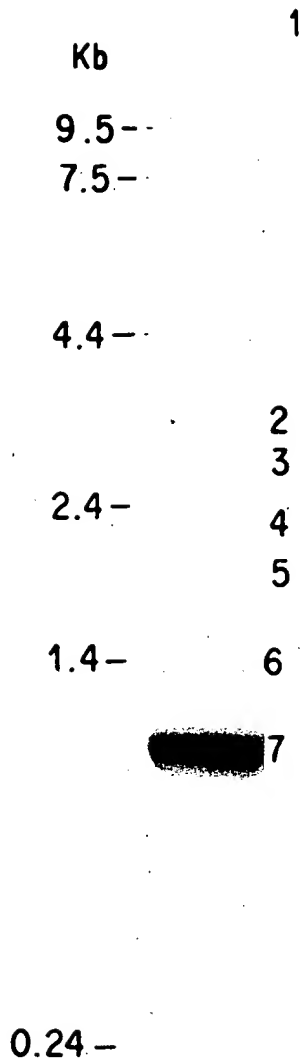


FIG.5

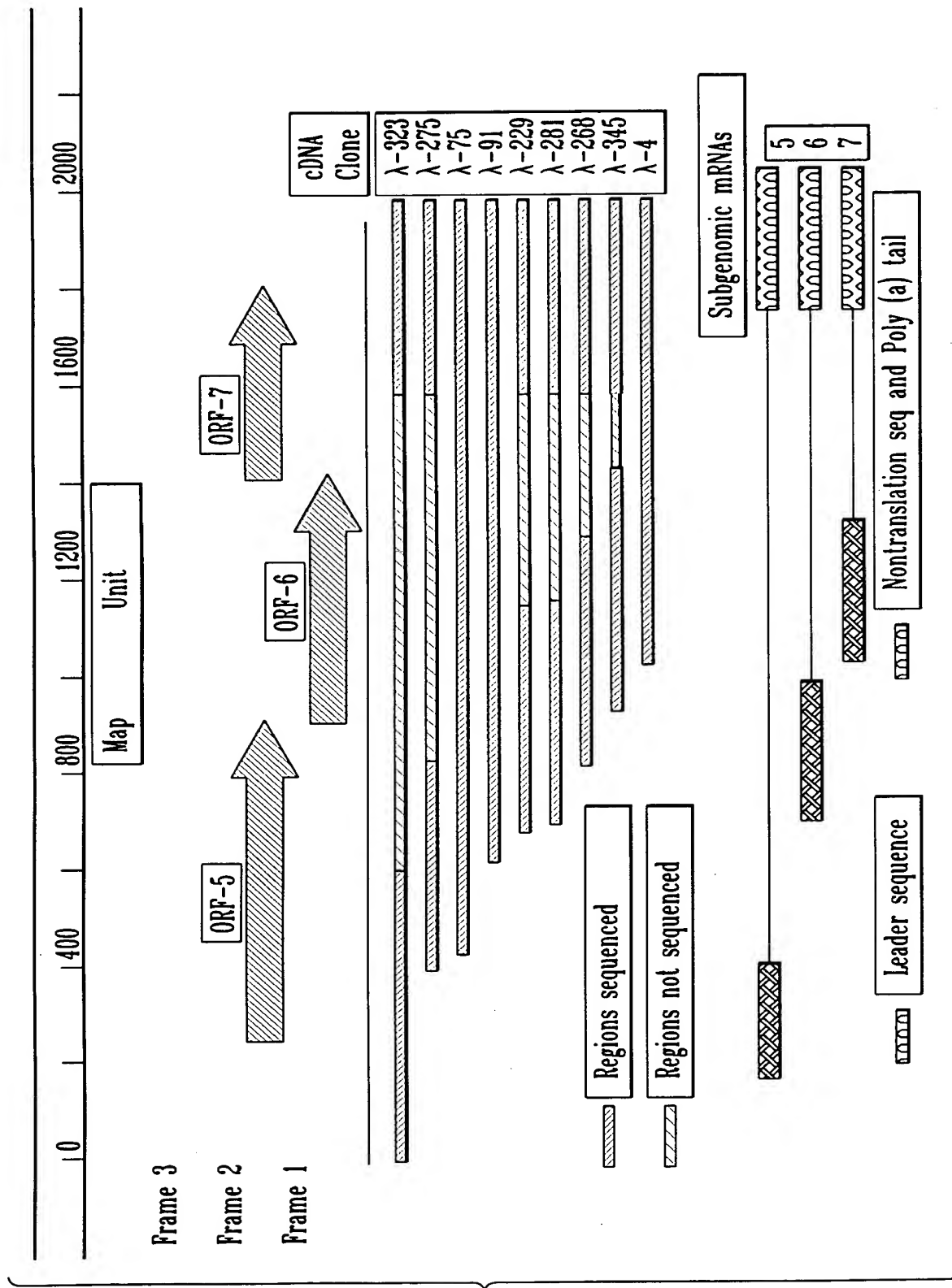


FIG. 6

GGCAGGCTTGGTGTCTCCAAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCTAGGGGATTCCGAAAGTCCCTCAGTCCCGCAGCGCGGATAGGG 100
 ACACCCGTGTATACACTGTACAGCCCAATGTTACCGATGAGAATTATTGCAATCCCTGATCTTCATGCTTCTTCTTGGCTTTTCTAIGCTTCTG 200
 AGATGAGTGAAAGGGATTAAAGGTGGTATTGGCAATGCTCAGGGATCGTGGCAGTGTGGCTCAACTTACCAGTTACGTCCAACATGTCAGGGAATT 300
 TACCCAACGTTCCTTGGTAGTTGACCATGTGGGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTAGCCTGCTTTTTTGGCATT 400
 CTTGTTGGCAATTGAAATGTTAAGTATGTTGGGGAATGCTTGACCGCGGGCTGTTGCTCGCAATTGCTTTTTTTGGTGTATCGTGGCGTCTGTTTT 500
 GTTGGCTGCTCAGCGCCACGGGAACAGCGGCTCAAAATTACAGCTGATTACAACTTGACGCTATGTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600
 AATTGACTGGGCAGTGGAGTGTTTTGTCAATTTTCCGTGTTGACTCACATTGTCTCTTATGGTGGCTCACACTAGCCATTCCCTGACACAGTGG 700
 TCTGGTCACTGTCTACCGCTGGGTTTGTTCACGGGGGTAAGTTCTGAGTAGCATGTACGGGGTCTGCGCCCTGGCTGGCTTGATTGGCTTCGTCATT 800
 AGGCTTCCGAAGAATTGCATGTCTCGGCTACTCATGTACCAGATATACCAACTTCTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGCGCTG 900
 TCATCATAGAGAAAGGGCAAGTTGAGGTGGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGAATGGTTCCGCGGCTACCCCTGTACCAGAGT 1000
 TTCAGCGGAACAATGGAGTCGTCCTTAGATGACTTCTGTCAATGATAGCAGGGCTCCACAAAGGTGCTCTTGGCGTTTTCTATTACCTACACGCCAGTGA 1100

DRF4 stop

 +1>DRF5 start

DRF6 start
 +1>
 ***DRF5 stop

FIG. 7A

TGATATATGCCCTAAAGGTGAGTCGGCGCCGACTGCTAGGGCTTCCTGACCTTTTGGCTCTCCCGAATTGTGCTTCACCTTCGGGTACATGACATTGGT 1200
 GCACCTTCAGAGTACAAATAAGGTGCGCTCAGTATGGGAGCAGTAGTTGCATCTCTTTGGGGGGGTGCTACTAGCCATAGAAACCTGGAAATTCATCACC 1300
 TCCAGATGCCGTTTGTGCTTGTAGGCGCGCAAGTACATTCTGGCCCTGCCACCACAGTTGAAGTGC CGCAGGCTTTCATCCGATTGCGGCAAAATGATA 1400
 ACCACGCAATTTGTCTCCGGGCTCCCGGCTCCACTACGGTCAACGGCACATTGGTCCCCGGTTAAAGGCTCGTGTGGGTGGCAGAAAGCTGTTAA 1500
 DRF7 start
 +1> ***DRF6 stop
 ACAGGGAGTGGTAAACCTTGTTAATATGCCAAATAACACCGGCAAGCAGCAGAGAGAGAGAGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600
 GCTGGGTAGATCATCGCTACCAAACCCAGTCCAGAGGCAAGGGACCGGGAAGAAAAAATAAGAGAAAAACCCGGAGAGCCCCCATTTCCCTCTAGCG 1700
 ACTGAAGATGATGTCAGACATCACTTACCCCTAGTGAGCGTCAATTGTGCTGCTCAATCCAGACCGGCTTAAATCAAGGCGCTGGGACTTGCACCC 1800
 ***DRF7 stop
 TGTCTAGATTCAGGGAGGATAAGTTACACTGTGGAGTTAGTTGGCTACGCATCATACTGTGGCGCTGATCCGGCTCACAGCATCACCCTCAGCATGATG 1900
 GGCTGGCATCTTGAGGGCATCCAGTGTGTAATTGGAAGATGCGTGGTGAATGGCAGTATTGACATTGTGCTCTAAGTCACCTATTCAATTAGGGC 2000
 GACCGTGTGGGGTAAGATTTAATTGGCGAGAACACACGGCGGAAATTAACCAAAAAA 2062

FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACAAATGGGGCGTTTCTTGACGCCACCTCTTGCCTTCTGGTGGCTTTTTTCTGTGTA--	13556
ISU-12-3' TERMINAL (426-1028)	-----ATGTTGGGGAAATGCTTGACCGCGCTTGTGCTGCAATTTGCTTTTTTGTGGTGATC	485
LELYSTAD SEQ (13484-14089)	---CCGCTTGTCTGTTTCTTTCGGATGTCACGGCCACAGGTCGACATACCATAA-C-ATAATAACTTGG	13624
ISU-12-3' TERMINAL (426-1028)	GTCCGCTCTTGTTTTGTGGGCTCTGAGCCCAACGGACACGGGCTCAATTTACAGCTGATTTACAACTTG	560
LELYSTAD SEQ (13484-14089)	ACGATATGGAGCTGAATGGGACCGACTGGTTTGTCCAGCCATTTTGTGGGCAGTGGAGACCTTGTGGTTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTTGAGCTGAATGGGACAGATTTGGCTAGGTAATAATTTGACTGGGCAGTGGAGTGTTTTGTCAATTTT	635
LELYSTAD SEQ (13484-14089)	CCGGTTGCCACTCATATCCCTCTCACTGGGTTTCTCACAAAGGCCATTTTGTGACGGCTCGGCTCTGGGCT	13774
ISU-12-3' TERMINAL (426-1028)	CGTGTGTTGACTCACATTTGCTCTTATGTTGGTCCCTCACACTACTAGCCATTTCTTGACACAGTCGGCTCTGGTACT	710
LELYSTAD SEQ (13484-14089)	GTAATCCACTGCAAGATTGTTTGGCGGGCGGTAGTACTCTCCAGCTCTACGGGCTTGTGCTTTCCGACGGCTTC	13849
ISU-12-3' TERMINAL (426-1028)	GTGTCTACCGGCTGGGTTTGTTCACGGGCGGTATTTCTGAGTAGCATGTACCGGCTCTGTGGCCCTGGCTGGCTTG	785
LELYSTAD SEQ (13484-14089)	GTATGTTTGTTCATCCGTGCTGTAAATAATTGCAATGGCTGCGCTATGGCGTACCGGTTTACCAACTTCATT	13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTGTTCATTAAGCTTGGCAAGCAATTGCAATGCTCTGGCTACTGATGACCAATATACCAACTTTCTT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTTTCATCGATGGAAGTCTCCAAATAGTGGTAGAAATAATTGGGCAAAAGCCGAGTCCGAT	13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGCAGACTCTATCGTTGCCGGTCCCTGTCTATCATATAGACAAAGGGGCAAAAGTTGAGCTCGAA	935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCACTCAAAATGTGCTCTCGAAGGGTTAAAGCTGAACCTTTGACAGGACTTCGGCTGA	14073
ISU-12-3' TERMINAL (426-1028)	GGTCACCTGATGAGCTCAAAAGAGTTGTGCTTGATGTTCCGGCGCTTACCCCTGTAAACAGAGTTTCAGGGGA	1009
LELYSTAD SEQ (13484-14089)	GCAATGGAGGCTTAG-----	14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTGGCTCTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 – 1413)	AAATCGACTCG	TCCTTAGATG	ACTTGTGTC	TCATAGGACG	GGTCCACAAA	AGGTGCTCTT	947
Lelystad seq (14077 – 14598)	-ATGG-GAGG	--CGTAGAG	ATTCTTTC	CGATCCCTATC	GGCGCACAAA	AGCTCGTCTT	14132
ISU 12/7a/3' terminal (888 – 1413)	GGCGTTTCT	ATTAACTACA	GGCCAGTGC	GATATATGCC	CTAAAGGTGA	GTCGGCGCCG	1007
Lelystad seq (14077 – 14598)	AGCGTTTACG	ATTAACTACA	GACGTATTAAT	GATATATGCC	CTAAAGGTGT	CACGGCGCCG	14192
ISU 12/7a/3' terminal (888 – 1413)	ACTCTTAGGG	CTTGTGCACC	TCTTGTCTT	CTTGAATGT	GGTTTCACT	TCGGGTACAT	1067
Lelystad seq (14077 – 14598)	ACTCTTGGG	CTGTGCACA	TCTTAATTAAT	TCTGAACGT	TCTTATTAAT	TCGGATACAT	14252
ISU 12/7a/3' terminal (888 – 1413)	GACATTCCTG	CACATTTCAGA	GTAAATTA	GGTGGGCTC	ACTATGGGAG	GAGTAGTTCG	1127
Lelystad seq (14077 – 14598)	GACATATCTG	CATTTTCAAT	CGACCAACCG	TGTGGACAT	ACCGTGGGCG	GTCTTGTCTG-	14311
ISU 12/7a/3' terminal (888 – 1413)	ACTCTTTCG	GGCGTGTACT	CAGC--CATTA	GAACTTGA	ATTTCATCAC	CTCCAGATGC	1185
Lelystad seq (14077 – 14598)	-CGCTTCTGT	GGGGTGTTTA	CAGCTTCACA	GAGTATGA	AGTTTATCAC	TTCAGATGC	14370
ISU 12/7a/3' terminal (888 – 1413)	CGTTTGTGCT	TGCTAGGCGG	CAAGTACATT	CTGGCCCTG	CCCACACCT	TGAAAGTGCC	1245
Lelystad seq (14077 – 14598)	AGATTGTGTT	GGCTTGGCG	GGATACATT	CTGGCCCTG	CCCATCAGCT	AGAAAGTGCT	14430
ISU 12/7a/3' terminal (888 – 1413)	GCAGCTTTC	ATCCGATTGC	GGGAAATGAT	AACCAACCAT	TCTCTGTCG	GGCTCCCGG	1305
Lelystad seq (14077 – 14598)	GCAGGTCTCC	ATTCAATCTC	AGCGTCTGCT	AACCAACCAT	ACGCTGTGAG	AAAGCCCGGA	14490
ISU 12/7a/3' terminal (888 – 1413)	TCCACTACG	TCAACGGCAC	ATTCTTCC	GGCTTAAAAA	GCCTCGTCT	GGCTGCCAGA	1365
Lelystad seq (14077 – 14598)	CTACATACG	TCAACGGCAC	TCTAGTACCA	GGATCTCGA	GCCTCGTCT	GGCTGCCAGA	14550
ISU 12/7a/3' terminal (888 – 1413)	AAAGCTGTTA	AAGAGGAGT	GGTAAACCTT	CTTAAATATG	CTAAATTA		1413
Lelystad seq (14077 – 14598)	CGAGCTGTTA	AAGAGGAGT	GGTAAACCTT	CTTAAATATG	CTAAATTA		14598

FIG.9

Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	ATGCCCGGTA AAAACGAG- GCCCAGAGAA AAAGAAAGT A-CAG----C ----- AT GCCAAATAC ACCGCAAGC AGCAGAAAGAG	14632 1434
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TCCCATCGGG AATGCCGAG CAGTCAATCA ATCTGGGAG TTGCTGGGTG AAGCAAGGGG GATGCCGAG CAGTCAATCA GTCTGGCAG ATGCTGGGT-	14681 1483
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CAATCATAAA GTCCACCGC CAGCAACCTA GCG--A-GG AAGGCGCAAA -AA-CATCAT CGCTACCAA AACCAGTCCA GAGCAAGCG ACCGG---GA	14728 1528
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAA-- ---- -CGTGAAG CACATTTTC CCTGGGTGG AAGAAAAITA AGAAGAAAAA CCGGAGAGAG CCGCATTTCC GTCTAGCGAG	14766 1578
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAC ATCCGCGACC ACCTACCCA CACTGACGC TCCGTTCCT TGAAGATGAT GTGAGACATC AGTTTACCCG TAGTGACCGT CAATTCTGTC	14816 1628
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TCCAATCCAT CCAGACCGGT TTCAATCAAG GCGCAGGAAAG -TCCGTTCCT TGTCTCAT AT CCAGACCGC TTAAATCAAG GCGCTGGGAG TTGCAAG-CCT	14865 1677
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TTTCATCCAG CGCAAGCTCA GTTTTCAGGT TCAGTTTAGT CTGCCGCTTG GTCAGATTCA GGGAGCAJAA GTTACACTGT GAGTTTAGT TTGCCTAGCG	14915 1727
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CTCATACAGT CCGCCCTGATT CCGGTGAGTT CTACATCCGC CAGTACGGT ATCATAGTGT CCGCCCTGATC CCGGTGACAG CATCAACCT-T CAG-CATGA-	14965 1774
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	GCAAGTTAA	14974 1774

FIG.10

ISU 12/7a/3' terminal (1775 – 1938)	TGGGCTGGCA TTCTTGAGGC ATCCAGTGT TTGAATTGGA	1814
Lelystad seq (14975 – 15101)	-----	14976
ISU 12/7a/3' terminal (1775 – 1938)	ACAAATCCGTC GTGAATGGCA CTGATTGACA TTGTCCTCT	1854
Lelystad seq (14975 – 15101)	TGACAGTCAG GTGAATGGCC GCGATTGGC TGTGGCTCT	15016
ISU 12/7a/3' terminal (1775 – 1938)	AAGTCACCTA TTCAATTAGG GCGACCTGT GCGGGTAACA	1800
Lelystad seq (14975 – 15101)	GAGTCACCTA TTCAATTAGG GCGATCACAT GCGGGTCATTA	15056
ISU 12/7a/3' terminal (1775 – 1938)	TTTAAATTTGG CGAGAACCAC ACAGCCGAAA TTAACAAAAA	1933
Lelystad seq (14975 – 15101)	CTTAATCAGG CAGGAACCAT GTACCCGAAA TTAACAAAAA	15096
ISU 12/7a/3' terminal (1775 – 1938)	AAAAA	1938
Lelystad seq (14975 – 15101)	AAAAA	15101

FIG. 11

TOP SECRET

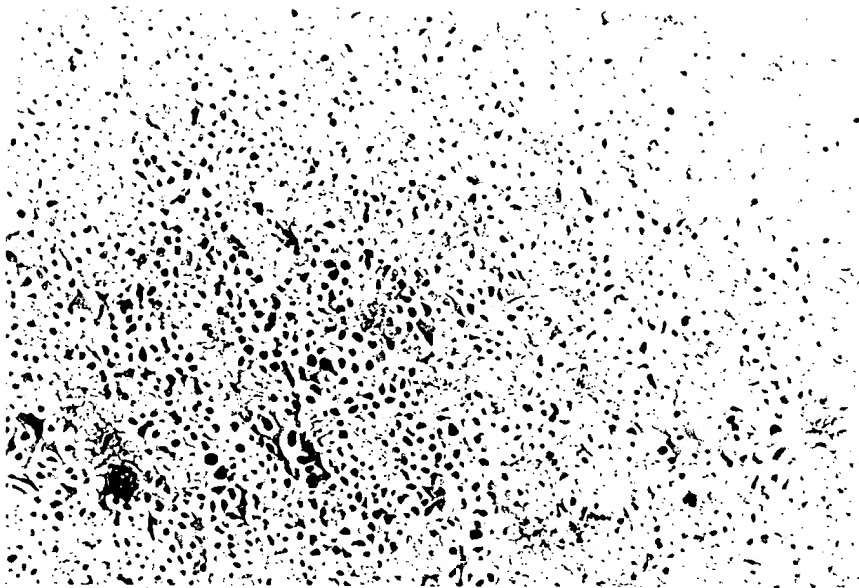


FIG.12

2025-04-13 14:00:00

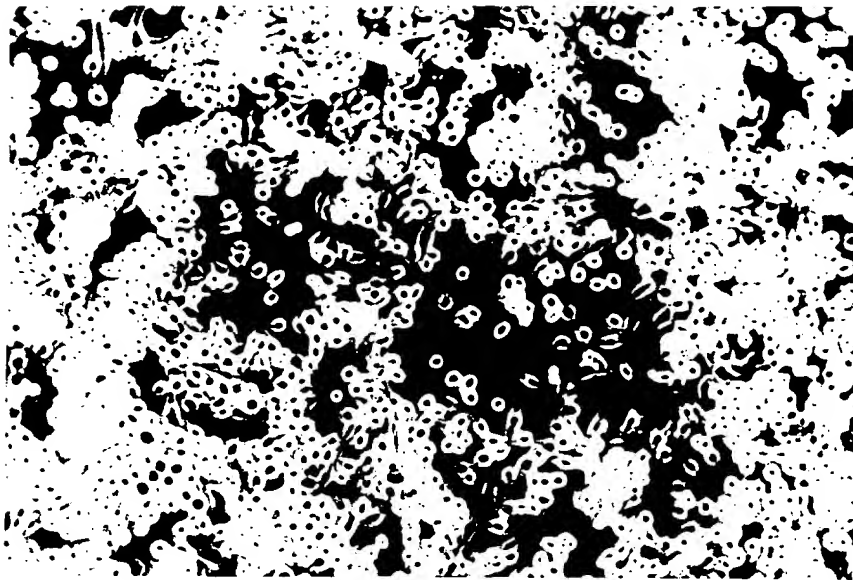


FIG.13

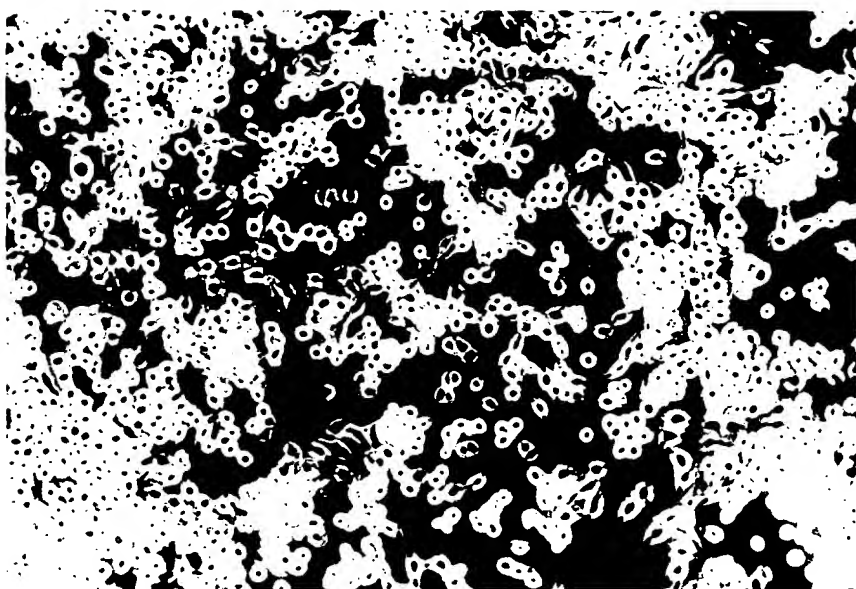


FIG.14



FIG.15

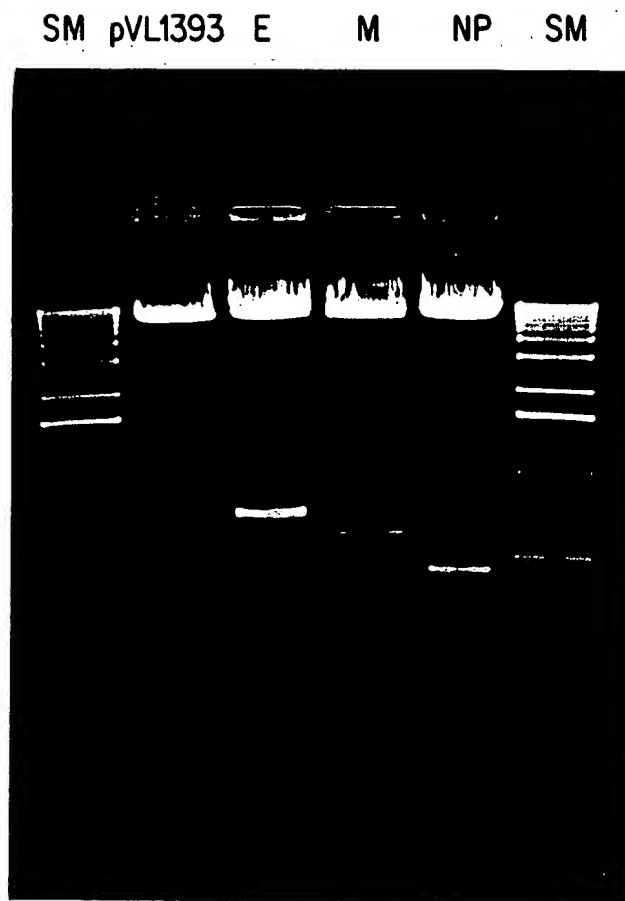


FIG.16

DRF 6 start
+ 1>

VR 2385	ALGGAGTCGTCCTTAGATGACTTCTGTGATGATACCGCGCTCCACAAAGTGCTCTGGCGTTTCTATTACCTACCGCCAGTGAATATAIGCCC	100
ISU-1894	... G..... C..... T..... I..... I.....	100
ISU-22	... G..... C..... I..... I.....	100
ISU-79	... G..... T..... T..... I..... A..... A.....	100
ISU-55	... G..... C..... I..... I..... C.....	100
ISU-3927	... G..... C..... C..... T. CA..... I..... I..... G..... T.	100
LV	... G--A--G.C....C..T.T.T.CA.C...CCT.TC.CG.....C.CG.GC.A.C...AGC..C.A....A..TA.A.....C...	97

VR 2385	TAAGGTCAGTCCGGCCGACCTGCTAGGGCTTCGACCCTTTGGTCTTCCTGAATTGGCTTCACCTTCGGGTACATGACATTGCTGCACCTTCAGAG	200
ISU-1894A.....	200
ISU-22	.G.....A.....	200
ISU-79A.T.....C.....A.....	200
ISU-55A..A.....A.....A.....	200
ISU-3927A.....A.T.T.....T.T.....G...	200
LV	.T.....TCA.....C.G.....GT.....A.CC.AA.A.T.....C..T.C.T.A.....A.....AT.....T....ATC	197

VR 2385	TACAATAAGGTCGCCCTCACAATGGGAGCAGTACTGCACCTCCTTTGGGGGGGTGTACTCAGC--CATAGAAACCTGGAAATTCATCACCCTCAGATGCC	298
ISU-1894	298
ISU-22A.....	298
ISU-79	298
ISU-55	C...C.....	298
ISU-3927	C...G.....C...T.C.....--	298
LV	C..C.CCGT...A..T..CC...G..T..T..C.--CCT.C.T...TTA...TT..C..GT.A...G..T...T.....A	295

FIG. 17A

VR 2385 GTTGTGCTTGGTAGGGCCGAAGTACATTCTGGCCCCCTGCCCCACCACGTTGAAAGTGGCCGAGGCTTCATCCGATTGGGGCAAAATGATACCCAGCATTT 398
 ISU-1894 398
 ISU-22 398
 ISU-79 398
 ISU-55T.....A..... 398
 ISU-3927G..... 398
 LVA.....TGC...T.A.CT.A.GTC...GA...A 395
 A.....T.GC...T....GGGA.....T.....A.....T.C.C...T.A.CT.A.GTC...GA...A 395
 VR 2385 TGTGCTCCGGGCTCCGGGCTCCACTACGGTCAACGGGCACATTGGTGGCCGGGTTAAAAAGGCTCGTGTTGGGTGGCAGAAAAAGCTGTTAAACAGGGAGTG 498
 ISU-1894G..... 498
 ISU-22T.....G..... 498
 ISU-79G..... 498
 ISU-55T.....G.....C..... 498
 ISU-3927T.....G.G.....A.....G..... 498
 LV C.CT.GA.AAAG...ACTA.AT.A.G.....TC.A.A.A.AC.TCGG.....C...C...A.CG.....GA..... 495

DRF 7 start

+ 1> *** DRF 6 stop

VR 2385 GTAACCTTGTAAATATGCGCAAAATACACCGGCA-AGCAGCAGAGAGAAAGAA-----GGGGGATGGCCAGCCAGTCAATCAGCTGTG 582
 ISU-1894C.....A..... 582
 ISU-22C.....A..T.- 582
 ISU-79C.....A..... 582
 ISU-55C.....A..... 582
 ISU-3927C.....A..... 582
 LVC.C.G...G.CGG...A.A.--.G.--.A.....AAGTACAGCTCCGAT...A.....A..... 591

FIG. 17B

VR 2385 CTTCACC-CTGTACAGATTCAGGGAGAGATAAGTTACACTGTGGAGTTAGTTTGGCTACGCATCATCTGTGCGCCATGATCCGGGTACACAGCATCACCC- 877
 ISU-1894T.....A.....T..... 877
 ISU-22T..... 877
 ISU-79T.....T..... 877
 ISU-55T.....G.....G..... 877
 ISU-3927 .C..T..T..A.....G.....T.....G..C.....G..C..... 877
 LVGT..G..T..TTCAGC...A..G..C...TTCAG..T.....TGC...GGTTGC...A.....T.....G..TT..TA..T..G 878

*** DRF 7 stop

VR 23 85 TCAG-CA-----TGA 886
 ISU-1894T..... 886
 ISU-22T..... 886
 ISU-79T..... 886
 ISU-55T..... 886
 ISU-3927T..... 886
 LV C...T..GGGTGCAAGT..A. 898
 ^^^^^^^^^^

FIG. 17D

VR 2385 DRF6 MESSLDFFCHDSTAPQVLLAFSITYTPVMIYALKVSRGRLGILLVFLNCAFTFGYMTFVHFQSTNKVALIMGAVALLMGVYSAIETWKTITSRCR 100
 ISU-1894 DRF6 .G.....I..... 100
 ISU-22 DRF6 .G.....I..... 100
 SIU-55 DRF6 .G.....I..... 100
 ISU-79 DRF6 .G.....Y.....I.....M..... 100
 ISU-3927 DRF6 .G.....N.....I.....E..R..... 100
 LV DRF6 .G-G...N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S..... 99
 PRRSV-10 DRF6 .G-G...N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S..... 99
 LDV-C DRF2 .G-G.-E..DATSWY.-IFI..L...IA.S..F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL...I..V..I.TLVKIVNMVWL... 96
 LDV-P DRF2 .G-G.-E..DATSWY.-I.I..L...IA.S..F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL...I..V..I.TLVKIVNMVWL... 96

VR 2385 DRF6 LCLLGRKYILAPAHVESAAAGFHP1AANDNH-----AFVRRPGSTIVNGTLVPGKSLVLGGRKAVKQGVNLYKY-AK 183
 ISU-1894 DRF6-----..... 174
 ISU-22 DRF6-----..... 174
 SIU-55 DRF6-----..... 174
 ISU-79 DRF6-----..... 174
 ISU-3927 DRF6-----.....R.....K.....-.. 174
 LV DRF6 ..C..R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR..R.....-GR 173
 PRRSV-10 DRF6 .C..R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR..R.....-GR 173
 LDV-C DRF2 ..F..S...PS..D-----TSDGRQSLTISLTI...K...L..Q..DFOR...K..SK.A..L..VS. 171
 LDV-P DRF2 ..F..S...PS..D-----TSDGRQSLTISLTI...K...L..Q..DFOR...K..SK.A..L..VS. 171

FIG. 184

VR 2385 DRF7 MPNNTGKQQRKK-----GDGQPVNQLCQMLGKIIAHQNSRGKGPCKKKKKNPEKPHPLATEDDVRAHFTPSERQLCSSIQIAFNQAGAGTCLLS 100
ISU-1894 DRF7 ...N.....-----Q.....Q.....
ISU-22 DRF7 ...N.....-----Q.....Q.....
ISU-79 DRF7 ...N.....-----Q.....Q.....
ISU-3927 DRF7 ...N.....K.....Q.....Q.....
ISU-55 DRF7 ...N.....K.....Q.....Q.....
VR2332 DRF7 ...N.....TEE.....Q.....Q.....
LV DRF7 ---A..N.SQ..KKSTAPM.N.....L..AM.KS.R.---QPR.GQA..K.....A..I..L.QT..S..Q.....AS.. 93
PRRSV-10 DRF7 ---A..N.SQ..KKSTAPM.N.....L..AM.KS.R.---QPR.GQA..K.....A..I..L.QT..S..Q.....PS.. 94
LDV-C DRF1 ..SQ.KK.GGAN.....AN.---.N.LISALLRNAG.--N..K.Q.K.-Q.-L..M.GPS.L.VM..N.V.M.R..LV.L...G.Q...V 85
LDV-P DRF1 ..SQ.KK.SGAN.....AN.---.N.LINALRNAG.--N..K.Q.K.-Q.-L..M.GPS.L.VM..N.V.M.R..LV.L...G.Q...V 85
EAV DRF7 ..ASRSRSP.AASF-----RN.R--RRQPTSYNDLLRMFG.-----MRVR.PPAQPTQAI.I.EPG.L..DLNQQ..ATLS.NV.RF.MI.H.SL.-A 83
^ ^ ^ ^ ^ ^ ^ ^

VR 2385 DRF7 DSGRISTYVESLPTHHTVRLIRVTASP-----SA 134
ISU-1894 DRF7 123
ISU-22 DRF7 123
ISU-79 DRF7 123
ISU-3927 DRF7P.---. 123
ISU-55 DRF7 123
VR2332 DRF7 123
LV DRF7 ..S..KV.FQ..M..VA.....STASQAGAS 128
PRRSV-10 DRF7 ..S..KV.FQ..M..VA.....STASQAGAS 128
LDV-C DRF1 ...G.NF..S.M...A...NAS.NS----- 115
LDV-P DRF1 ...G.NF..S.M...A...NAS.NS----- 115
EAV DRF7 ..A.GLT...SW-V..KQIQ.KVAPP.G.----- 110
^ ^ ^ ^ ^

FIG. 18B

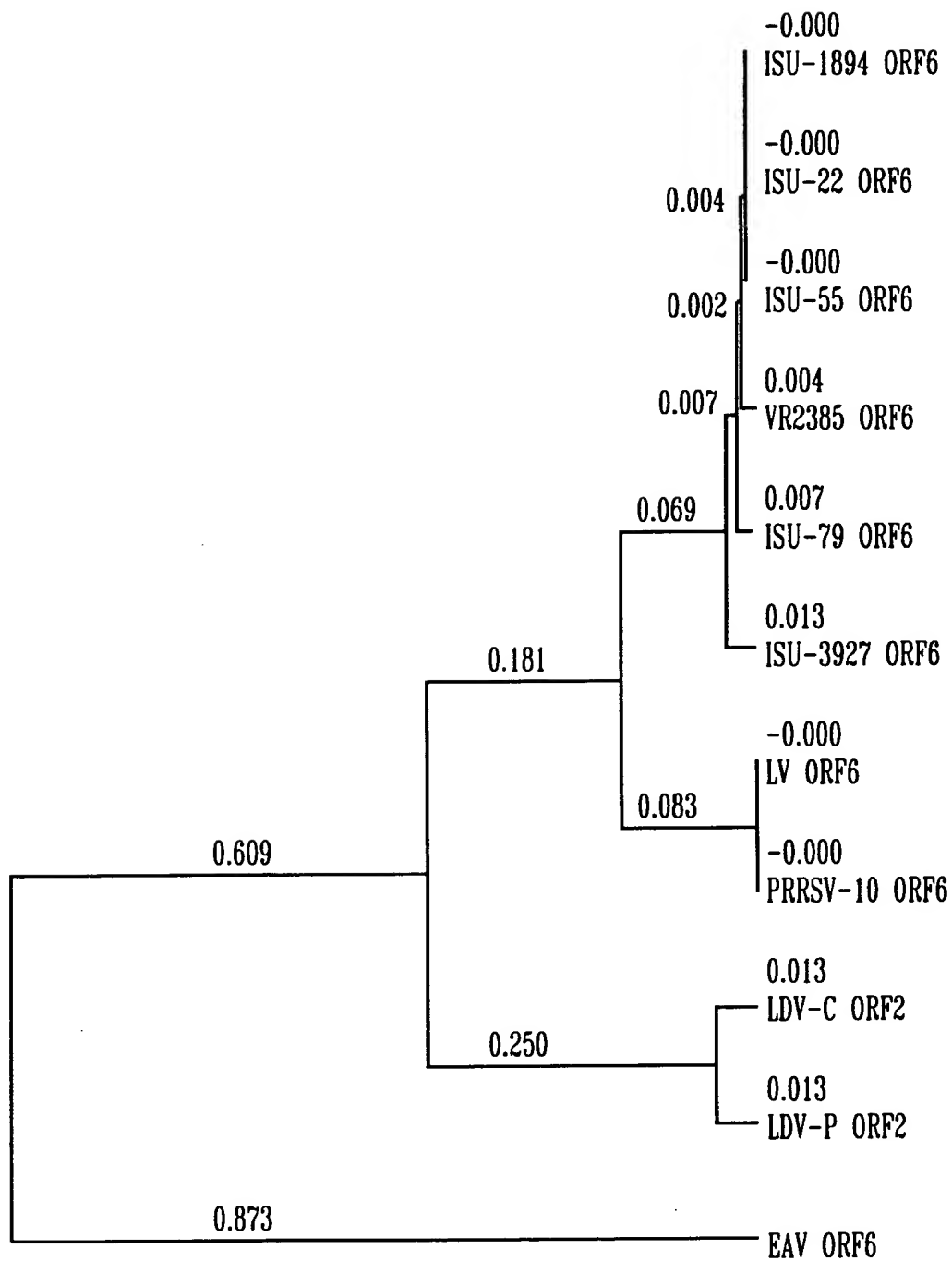


FIG. 19A

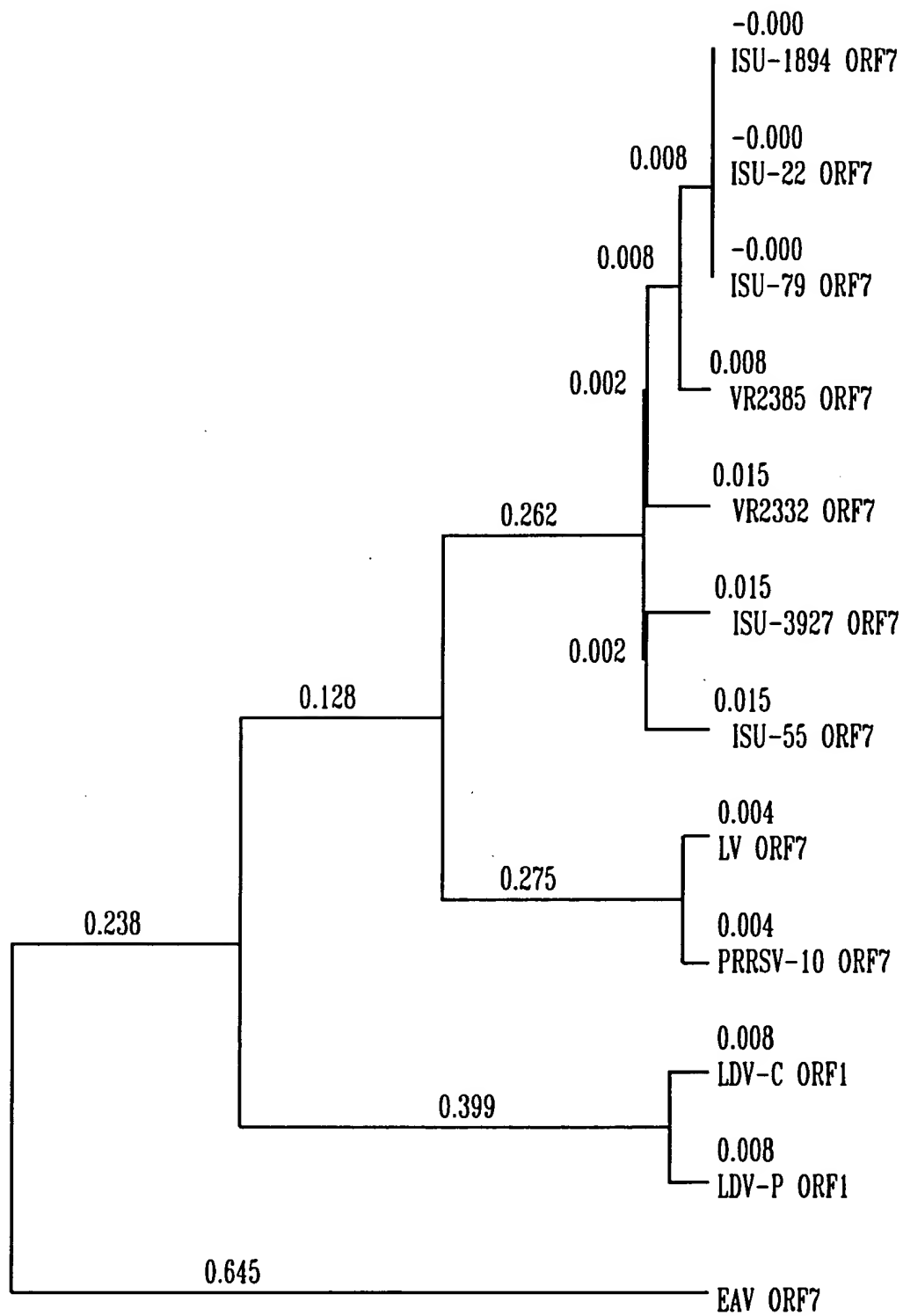


FIG. 19B

+ Start DRF2

100 CCTGAATTGAGATGAAATGGGGTCTATGCAAAAGCCTTTTGGACAAAATTGGCCAACCTTTTGGGATGCTTTCACGGAGTTCCTGGTGTCATTGTTGAT

200 ATCATTATATTTTGGCCATTTTGGCTTCACCATCGCAGGTGGCTGGTGGTCTTTTGGCATCAGATTGGTTTGCCTCCGCGATACTCCGTGGCGGCC

300 CTGCCATTCACTCTGAGCAATTACAGAAAGATCCTATGAGGCCTTTCTCTCTCAGTGCAGGTGGACATTCACCACCTGGGGAACAAACATCCTTTTGGGGA

400 TGCTTTGGCACCATAAGGTGTCAACCCTGATTGATGAATGGTGTCCGCTCGAATGTACCGCATCATGGAAAAGCAGGACAGGCTGCCTGGAAACAGGT

500 AGTGAGCGAGGCTAGGCTGTCTCGCATTAGTAGTTGGATGTGGTGGCTCATTTTCAGCATCTTGGCGCCATTGAAGCCGAGACCTGTAAATATCTGGCC

600 TCTCGGCTGCCCATGCTACACCACCTGGCGATGACAGGGTCAAAATGTAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTGCTGTTTTCCCAACCC

+ Start DRF3

700 CTGGTTCCCGGCCAAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCCTCTCTATATTTCCCTCTGTTGCAGCTTCCTTTTGTGTTGT

*** Stop DRF2

800 GCTGTGTTGGGGTCCAAATGCTACGTACTGTTTGGTTCCGCTGGTAGGGCAATTTTCTTTCGAATCAGGTTGAATTACACGGTGTGCCGC

900 CTTGCCTCACCCGGCAGCGCGCAGAGGCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATCGATGTGGGAGGACGATCATGATGA

1000 ACTAGGTTTGTGGTGGCGTCTGGCCCTCCAGCGAAGGCCACTTGACCAGTGCCTACGGCTGGTTGGCGTCCCTGCTCCCTTCAGCTATACGGCCAGTTC

1100 CATCCCGAGATATTCGGGATAGGGAAATGTAGTTCGAGTCTATGTTGACATCAAGCACCAATTCATTTGGCGTGTTCATGATGGGCAGAACACCACCTTGC

FIG. 20A

+ Start DRF4
 CCCACCATGACAACATTTACGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTTCACCTAGAATGGTGCGTCCCTTCTTTC 1200
 CTCCTGGTTGGTTTTAAATGTCCTCTGGTTTCTCAGGGCTTCGCCTGCAGGCCATGTTTCAGTTCGAGTCTTTTCAGACATCAAGACCAACACCACCGCAG 1300
 *** Stop DRF3
 CGGCAGGCTTTGCTGCTCCAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCTGAGGCGATTGCGAAAGTCCCTCAGTGGCCGACGGGATAGG 1400
 GACACCGGTGATATCACTGTCACAGCCAATGTTACCGATGAGAAATTATTGCATTCCCTCTGATCTTCTCAIGCTTTCCTTGGCTTTTCTAIGCTTCT 1500
 GAGATGAGTGAAAAGGGATTTAAGGTGGTATTTGGCAATGTGTAGGCCATCGTGGCAGTGTGCGTCAACTTCACCAGTTACGTCCAACATGTCAAGGAAT 1600
 TTACCCACGTTCCCTGGTAGTTGACCATGTGGCGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTTAGCCTGTCTTTTACCAT 1700
 *** Stop DRF4 + Start DRF5
 TCTGTTGGCAATTTGAATGTTTAAGTAAGTGGTGGGAAATGCTTGACCGGGGCTGTTGCTCGCAATTGCTTTTTTATGGTGATCGTGCCGCTTGTT 1799

FIG. 20B

Consensus	ATGMAATGGGGTCWMTGYRRAGCCTTTTIGAYAAAATYRCCARCTKTTYGTGGAYGCTTCACKGAGTTCYTKGKWSYRTKGTGATATRYYYATWT	100
VR2385 DRF2	... A, ..., TA, , CAA, ..., C, ..., TG, ... A, T, T, ..., T, ..., G, ..., T, G, , GTCCA, T, ..., CATT, ... A, ,	100
LV DRF2	... C, ..., AC, , TGG, , -----T, ..., CA, ... G, G, C, ..., C, C, ..., T, ..., TAGTG, G, ..., TGCC, ... T, ,	91
Consensus	YYTKGCCATWYTGTTGGSTTACCRTCGCAGGWTGGYTRSTGGTCTTTYKMYTCAGAKTGGTTTGCTCCGGMTWCTCCGKCGGCGCTGCCATTAC	200
VR2385 DRF2	TT, G, ..., TT, ..., C, ..., A, ..., T, C, GG, ..., TGCA, ..., T, ..., A, A, ..., G, ..., C, ...,	200
LV DRF2	CC, T, ..., AC, ..., G, ..., A, ... T, AC, ..., CTC, ..., C, T, ..., T, ..., T, ...,	191
Consensus	TCTSMSSAAYTAYMGAAGRTCTATGARGCTTKYTSYCYMASTGCMRRSYGGAYAKTCCACAMTKKSARYYAARCAAYCCWTTGGGKATGYTTTGGCA	300
VR2385 DRF2	... GAGC, ... T, CA, ... A, ... G, C, ... TC, CT, TC, G, ... CAGGT, ... C, T, ... -C, GG, G, ACT, ... A, T, ... G, ... C, ...	299
LV DRF2	... CCCG, ... C, TC, ... G, ... A, G, ... GT, GC, CA, C, ... AGACC, ... T-G, ... A, TT, C, GTC, ... G, C, ... A, ... T, ...	290
Consensus	CCATRMGAGTKTCMMMCYTGATTGATGARATGGTSTCKCGTCGMATKTACCRSAYCATGGAAAMWKCAGGWCARGCKGCTGGAAARCAGGTGTRGKYGA	400
VR2385 DRF2	... AA, -, G, AAC, C, ..., A, ..., G, ... A, G, ... GC, T, ..., A, AG, ... A, G, ... T, ..., A, ... A, GA, C, ,	398
LV DRF2	-, GC, ..., T, CCA, T, ..., G, ..., C, T, ..., AG, C, ..., C, TT, ... T, A, G, ..., G, ..., G, TG, T, ,	389
Consensus	GGCYACGCTSTCWCGMAKYWGTCAGGKYTSGARTRGTRKRCATTTTCARCAYCTKCCGCMRTKGARGCSGAKWCTGYMRMTWTCTSRSCTCWCGR	500
VR2385 DRF2	... T, ..., G, T, C, TTA, , -, TT, G, ... G, G, GG, ..., T, G, T, T, ..., CA, T, A, C, ... GA, C, , TAAA, A, ... GGC, ... T, G, ,	496
LV DRF2	... C, --, C, A, A, A, GCT, ..., GC, C, ... A, A, TA, ..., C, A, C, ... AG, G, G, G, TT, T, CCGC, T, ... CAG, ... A, A, ,	487

FIG. 21A

Consensus	TSSYSATGCTAMAMMAYCTGYGCAYGWAAGGTCAAATGTRASCMTASGTAAYASYACKTTIGRAYCRSGTGKVGCTCRITYTTCCCMACSCCWGGTW	600
VR2385 DRF2	, GCCC.....C. CC. C., C., C., T. AC.....A. C. A., GT., T., T. GT., T., A. T. AG., ... TT., ... -G. T., ... A., C., T., ... T	595
LV DRF2	, CGTG.....A. AA. T., -T., -C. TT--., -, -,, G. G. C., CA., C., C. CC., G., G. C. GC., -, GA., ... A. C., ... C., G., A., ... A	580
Consensus	CSMGGCCMAAGYTKMNYGATTCMRRCATGGCTMATMRSTGTRCAYKCYTCYATWTTTCCCTCTGKGCWKCTCKTACYYTKTYRTWGTGCTKTG	700
VR2385 DRF2	, CC.....A., C. TCAT.,, CAG.....A., AGC., ... A., TT. C., T., A.,, ... T., AG. T., ... TG., ... TC. T., ... TG. T., ... G.,	695
LV DRF2	, GA., ... C., T. GACC.,, AGA.,, C., CAG., ... G., CG. T., C., T.,, ... G., TT. A., ... GT., ... CT. G., CA. A., ... T.,	680
Consensus	GYTKCGRRTTCCARYKCTACGYWMGTGTTTTTGTTTCCRYTGGYMRSGGCAAYWWTCTTCGARTSACGGTGA	776
VR2385 DRF2	, T. G., GG., ... ATG., ... TAC.,, ... GC., ... TTAGG., ... TTTT., T., ... A., C., ... , 771	771
LV DRF2	, C. T., AA., ... GCT., ... CTA.,, ... AT., ... CCCAC., ... CACA., A., ... G., G., ----- 750	750

FIG. 21A.1

Consensus ATGGCTMATMRSTGTRCAYKCYTCYATWTTTCCTCTGTGKGCWKWCCTCKTACYYTKTYRTWGTGCTKGGYTKGRRTTCCARYKCTACGYWMTGTT 100
 LV DRF3 C.. CAG.. G.. CG.. T.. C.. T.. G.. TT.. A... GT... CT.. G.. CA.. A... T... C.. T.. AA... GCT... CTA... 100
 VR2385 DRF3 A.. AGC... A.. TT.. C.. T.. A.. T.. AG.. T... TG... TC.. T.. TG.. T... G... T.. G.. GG... ATG... TAC... 100

Consensus TTTGGTTTCCTRYTGGYMRSGGCAAYWYWCWTTTCGARCTSACRS TSAAYTACACSRTRTGC MYGCCYTGYYACCMGKCAAGCRGCTCGCMRARGSCT 200
 LV DRF3 AT... CCCAC... CACA.. A... G.. G.. CA.. C.. C... CA.. A... AT... C.. TTCT... A.. T... G... G... CA.. A.. G.. 200
 VR2385 DRF3 GC... TTAGG... TTTT.. T... A.. C.. GG.. G.. T... GG.. G... CC... T.. CCTC... C.. G... A... A... -... AG.. G.. C... 199

Consensus ACGARCCCGYMGKWCMTKTGGTGCARRATAGGGCATGAYMGRGTGTGRGGAGSRGYCATGATGARYTAGKWWTGTCSRTSCCGTCYGGSYWCKMCA 300
 LV DRF3 -... G... TC.. TAA.. A.. G... AA... CA.. G... A... CGT... C... GT... -... TTAA... CA.. C... C... C... GTA.. GA.. 298
 VR2385 DRF3 A... CA.. GTC.. C.. T... GG... GC... TC.. A... G... GAC... T... AC... GGTT... -GG.. G... T... CCT.. TC... 298

Consensus sRCGAMKSMMACTTGACSRGKMTTAYGCTGGYTGCKTYYTGTCCCTYWSCYATRCGGCCCARTTCCATCCSGAGWRTTCGGGATAGGGAATGIGWS 400
 LV DRF3 A.. --CTCAA... -GG.. TA... T.. T... C... T.. TTT... TTC... CG... A... G... T.. G... TC 395
 VR2385 DRF3 G... AGGCC... CA.. GC... C.. C... T... G.. CCC... CAG... TA... G... C... A.. A... AG 398

Consensus KCGMGCTIWTGKACAWSMRRCACCARTTCATTGTGCGYGWKCATGATGGRCSAAYVCMACCKTRYCYMMCSRWSACAACATYTCMGCMKTRYWTSMG 500
 LV DRF3 G.. C... TC... G... AGCGA... G... T... C.. AG... A... A... C... TT.. A... G.. AT.. TAC.. GGAC... C... C... AT.. ATA.. GC.. 495
 VR2385 DRF3 T.. A... AT... T... TCAAG... A... C... T.. TT... G... G... CA.. C... T.. GC.. CCA.. CATG... T... A... CG.. GCT.. CA.. 498

FIG. 21B

Consensus	RCMTATTACCASCAYCARRTMGACGGGGCAATTGGTTYCAYYTRGAATGGSTGCGKCCMYCTCTTTCYTCYTGGTGGTKYTMAYRTMTCWTGTTTC	600
LV DRF3	G. A. C. C. . AA. A. C. TT. G. C. G. AC. T. C. . C. GC. C. . CA. A. A.	595
VR2385 DRF3	A. C. G. T. . GG. C. T. CC. A. G. T. CT. C. T. . T. TT. A. . TG. C. . T.	598
Consensus	TSAGGCGTTCCGCTGYAAGCCMTGTTTCWSKWCGRMRTCTWTCAGAYATYRAGACCAACACACACCGCRGCKGCMGGYTTYRYKGTCTCTYCARGACATCART	700
LV DRF3	. G. T. C. TCGA. . CA. . A. T. TG. G. T. C. . T. . CATG. T. G. A. .	695
VR2385 DRF3	. C. C. A. AGTT. AG. . T. C. CA. C. A. G. A. C. . TGCT. C. A. G. .	698
Consensus	TGYTTYMGRMTCACGGSRWCTCRGCAGCKCAWGAGRMRTTTCCTTCGSAAGTCGYCYCARTGYCGYGAMGCGWVRGTACTCCCCAGTACATCACGA	800
LV DRF3	. . TT. CC. A. C. GGT. . . A. G. A. . . AAA. G. T. C. A. . T. . A. C. . TCG.	795
VR2385 DRF3	. . CC. TA. G. A. . ---, CAA. . . G. . --, T. -T. . . GCG. -----, . . . C. -C. T. G. . C. . C- . C. G. . ATA. -----	765
Consensus	TAA	803
LV DRF3	. . .	798
VR2385 DRF3	---	765

FIG. 21B.1

Consensus	M, WG, C., K., L., W., L., P, CL, SPSQ, G, WSF, S, WFAPR, SVRALPFTL, NYRRSYE., L., C., D, P., KH	100
LV DRF2	. Q., H, GV, SASCSWTPS, SSSLV, LI-----, PF., ---, Y., G., D, Y., F, E., P., GL, PN, RP, V, QFAV., .	90
VR2385 DRF2	. K., L., --, ----AFLTK, AN-FL, MLSSSSWCP, LI., YFW, F., A., V, W., A, D., Y., S., AF, SQ, QV, I, TWGT., .	93
Consensus	PLGM, WH., VS, LIDEMVSRR, Y., ME., GQAAWKQVV, EATL., S, LD, V, HFQHLAA, EA., C., L, SRL, ML., L., NV., YN, TL., V.,	200
LV DRF2 F., MR., H., I, QT., HS., G., TKL, G., I, T., V., DS, RF, S., V., KN, AV--G., SLQ., T., DR, ELI	188
VR2385 DRF2 L., HK., T., M, RI., KA., S., SRI, S., V, A., I., ET, KY, A., P., HH, RMTGS., TIV., S., NQ, FAV	193
Consensus	FPTPG, RPKL, DF, QWLI, VH, SIFSSVA, S, TLF, VLWLR, P, LR, VFGF, W., A.,	264
LV DRF2 T., T., R., S., A., S, V., I., I, A., Y., H, PT, ---THSS	249
VR2385 DRF2 S., H., Q., A., S., A, C., V., V, M., T., R, LG, IFLNSNR-	257

FIG. 22A

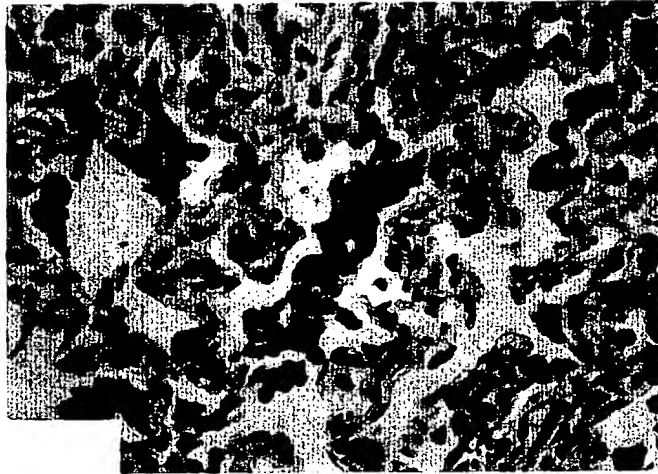


FIG.23

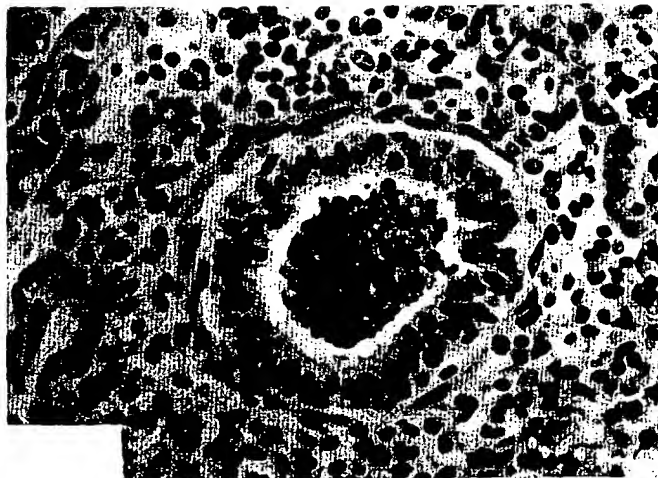


FIG.24

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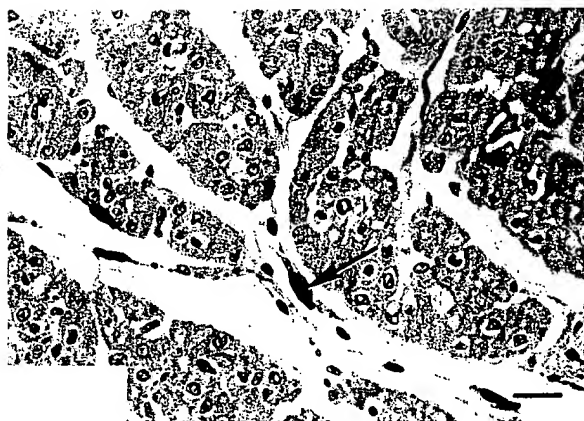


FIG.25

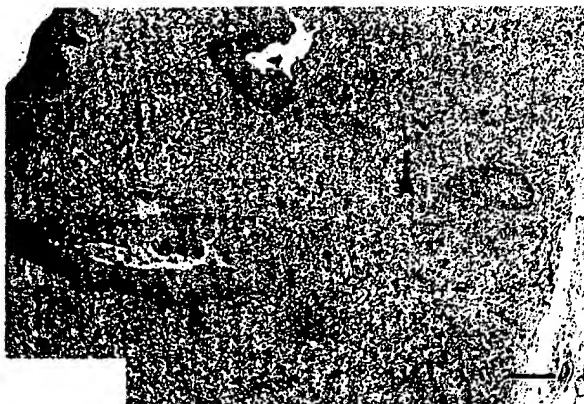


FIG.26

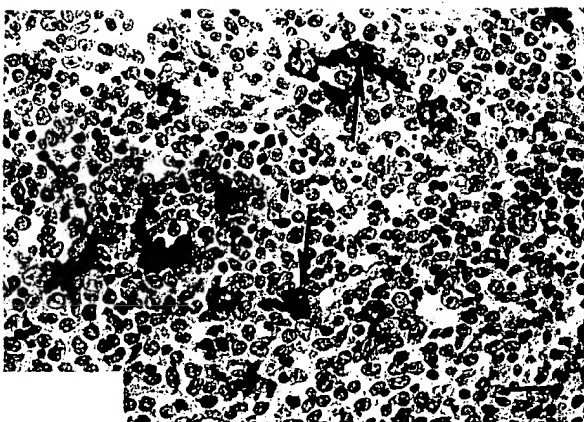


FIG.27

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FIG. 28A



FIG. 28B



FIG. 28C

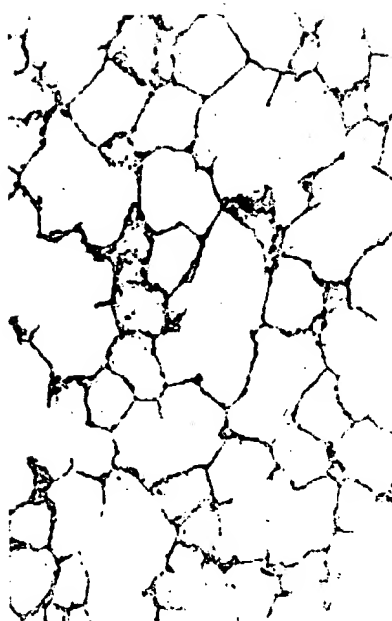


FIG. 29A

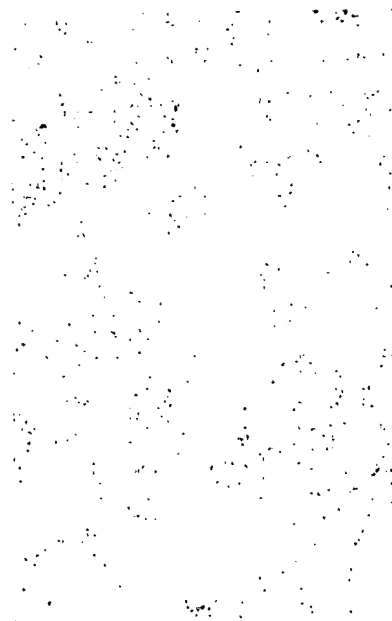


FIG. 29B



FIG. 29C

FIG. 28A

22 55 79 1894 3927

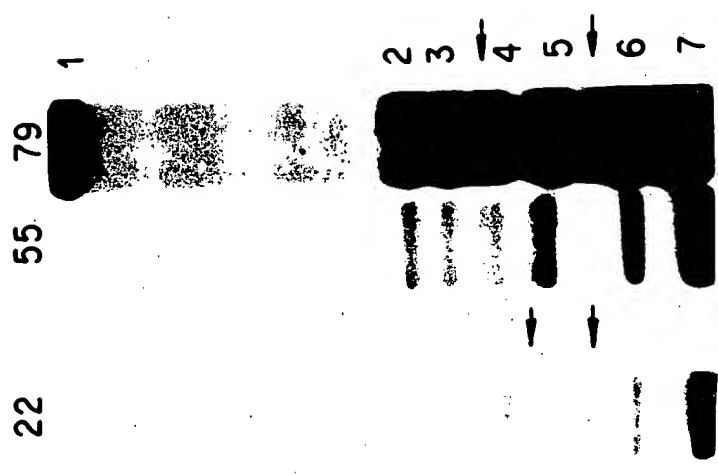


FIG. 30A



FIG. 30B